```
 M P S R C H  (TM)
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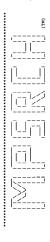
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MPsrch_ln   n.a. : n.a. database search, using Smith-Waterman algorithm

Run on: Wed Sep 8 13:40:50 1999: MasPar time 75.04 Seconds
                                        916.624 Million cell updates/sec

Tabular output not generated.

Title: >US-09-133-119-2
Description: (1-321) from US09133119.seq
Perfect Score: 321
N.A. Sequence: 1 GACATCTTGCTGACTCAGTC..........GGACAAATTGGAAGTAAAA 321
Comp: CTGTAGAACGACTGAGTCAG..........CCTGTTTAAACCTTCATTTT

Scoring table: TABLE default
               Gap 6

Nmatch STD: 0   Dbase 0: Query 0

Searched: 271905 seqs, 107135622 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: n-geneseq35
               n:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
               8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
               14:part14 15:part15 16:part16 17:part17 18:part18 19:part19
               20:part20 21:part21 22:part22 23:part23 24:part24
               29:part29 30:part30 31:part31 32:part32 33:part33
               34:part34 35:part35 36:part36 37:part37 38:part38 39:part39
               44:part44 45:part45 46:part46 47:part47 48:part48 49:part49
               54:part54 55:part55 56:part56 57:part57 58:part58 59:part59
               59:part59 60:part60

Statistics: Mean 8.015: Variance 4.693: scale 1.708

              Pred. No. is the number of results predicted by chance to have a
              score greater than or equal to that of the result being printed,
              and is derived by analysis of the total score distribution

              SUMMARIES

         Query
Result Match Length DB   ID   Description   Pred. No.
No.   Score
---- ----- ------ --- ------ --- -----------
 1   321   100.0   321 37 V03615   Coding sequence for 1   9.02e-208
 2   291   90.7   321 44 W97441   Humanised CA2 light-c   4.54e-186
 3   291   90.7   321 35 W90300   Insert-coding for lig   4.59e-186
 4   286   89.1   321 40 V12262   Monoclonal antibody   1.91e-182
 5   286   89.1   321 30 X43243   B-R10 MAb L-chain V   2.17e-107
 6   277   86.3   321 44 V26570   Anti-gp54 MAb 48-127   6.04e-176
 7   277   86.3   321 22 710   Light chain variable   1.68e-174
 8   275   85.7   321 17 Q40463   FV(TU05).   1.68e-174
 9   275   85.7   321
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 10   274   85.4  274    10  Q48766   Monoclonal antibody B   8.84e-174
 11   273   85.0  273     8  U01951   Mouse antibody cDNA     4.64e-174
 12   273   85.0  381    32  T49338   cDNA encoding kappa l   4.66e-173
 13   273   85.0  416    32  T49342   cDNA encoding kappa l   4.66e-173
 14   272   85.0  300     3  Q20306   B cell hybridoma P1.5   2.45e-172
 15   271   84.1  318    48  V54798   DNA encoding the ligh   6.80e-171
 16   270   84.1  322     6  Q36614   scFV chimeric heavy-b   3.58e-170
 17   270   84.1  322     6  Q36615   Anti-IL2R-beta antibo   3.58e-170
 18   269   83.2  486     7  Q43384   L-chain V-region of m   9.22e-169
 19   267   83.2  265     6  Q43384   Light chain-V regio f   2.75e-167
 20   265   82.6  2070   24  T42035   Plasmid pWVII-225 fr    2.75e-167
 21   265   82.6  2793   24  T42039   Plasmid pMS238-5-225    2.75e-167
 22   265   82.6  2863   24  T42041   Plasmid pSWZ07-225 fr   2.75e-167
 23   265   82.6  3177   24  T42041   Plasmid pMS240-5-225    2.75e-167
 24   253   78.8  720     7  Q40462   PV(TU27).               1.22e-158
 25   211   65.7  324    58  V71798   Murine vitronectin al   2.46e-121
 26   201   62.6  486     7  V71798   hIL2R Ab L_chain V re   2.76e-115
 27   193   60.1  5238   29  Q04654   Sequence of mouse Vka   4.79e-110
 28   185   57.6  324    23  T33446   Plasmid pWTll encodi    5.36e-110
 29   185   57.6  324    23  V71800   EGF receptor chimeric   5.36e-108
 30   182   56.6  182    23  V71800   Humanised anti-light-   4.79e-107
 31   181   56.4  338    58  V71802   Vitronectin alpha-r b   4.47e-107
 32   161   50.2  315    59  V71803   Light chain coding se   1.88e-105
 33   161   50.2  315    59  V71803   Vitronectin alpha-r v   1.88e-105
 34   160   49.8  315    59  V71805   JK gene segment.        9.56e-93
 35   133   41.4  133     1  Q71872   Human.seat anti-alpha   9.56e-93
 36   133   41.4  924    10  Q71879   Sequence coding human   3.59e-73
 37   122   38.0  1204   22  Q78772   IgG light-chain varia   1.77e-65
 38   120   37.4  812    25  T37180   DNA fragment VK55.3;    3.98e-64
 39   120   37.4  812    25  Q78852   Human V-kappa gene VK   4.38e-64
 40   120   37.4  812    50  V38182   Human DNA fragment VK   4.38e-64
```

                                                  ALIGNMENTS

```
RESULT
ID    V03615. standard; cDNA; 321 BP.
AC    V03615;
DT    22-APR-1998  (first entry)
KW    kappa light chain variable region used in chimeric Ab;
KW    Tumour necrosis factor; human; hTNF; rheumatoid arthritis; malignancy;
KW    anti-TNF chimeric antibody; inhibitor; therapy; rheumatoid arthritis; infection;
KW    chimeric antibody; human antibody; light chain;
KW    neurodegenerative disease; variable region; se:
OS    Mus sp.
PN    US5656272-A.
PP    15-DEC-1997.
PF    04-FEB-1994; US-192102;
PR    18-OCT-1994; 324792-99
PR    18-MAR-1991; US-670827
PR    18-MAR-1991; US-853606
PR    18-MAR-1991; US-01006
PR    29-JAN-1992; US-01006
PA    02-FEB-1994; US-013413
PR    02-FEB-1994; US-192093
PR    04-FEB-1994; US-192102;
PR    04-FEB-1994; US-192102;
PA   (DRW / UNIV NEW YORK MEDICAL CENT.)
PT   Daddona P. Chrayeb D. Le J. Siegel.
PT   Olcese J.
DR   WPI; 98-051431/05.
DR   P-PSDB; W04820.
PS   Claim 15; Column 99:100; 99pp; English.
CC   This sequence represents the coding sequence for the variable light chain
CC   of a mouse antibody. This sequence can be used as part of the chimeric
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Left column

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CC   antibody used in the method of the invention. The method of the invention
CC   is for treating rheumatoid arthritis in a human, and comprises
CC   administering to the human an effective tumour necrosis factor- (TNF)
CC   inhibiting amount of an anti-TNF chimeric antibody (Ab), where the
CC   anti-TNF chimeric Ab comprises a non-human variable region of a TNF
CC   antigen binding portion of the variable region, and a human constant
CC   region. The method can be used for in vitro, in situ and/or in vivo
CC   diagnosis of mammalian cells, tissues or pathologies associated with the
CC   presence of TNF. The Ab used in this method can also
CC   be used for removing TNF from a solution or cells, inhibiting one or more
CC   biological activities of TNF in vitro, in situ or in vivo. Such methods
CC   can include treatment methods of the invention for alleviating symptoms
CC   or pathologies involving TNF, such as bacterial, viral or parasitic
CC   infections, cachexia, graft rejection, autoimmune diseases,
CC   malignancies and/or neurodegenerative diseases.
SQ   Sequence 321 BP; 83 A; 72 C; 77 G; 89 T;

Query Match            100.0%;  Score 321;  DB 37;  Length 321;
                       Best Local Similarity 100.0%;  Pred. No. 9.02e-208;
Matches  321;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Db    1 gcacctctgactcagcctccaccgtgtcagggagaaagtcagt 60
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Qy    1 GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGACTCCAGGAGACAGAGTCAGT 60

Db   61 tcctctccaggccagcctccatcctgtctgcaacaccggagacc 120
        ||||||||||||||||||||||||||||||||||||||||||||
Qy   61 TTCTCCTGCAGGGCCAGCTCAGGTTCTCGAGTCATGTCTGGAATCCTTCC 120

Db  181 agttcagcggcagtgatccaacgattacccaccgctcctggctcctc 240
        |||||||||||||||||||||||||||||||||||||||||||||||
Qy  181 GAAGATATTGCAGATTATTACTGTCAACAAGTCATAGCTGCCATCAAGGTCAT 240

Db  301 ggacaaattggaagtaaaa 321
        ||||||||||||||||||||
Qy  301 GGGACAAATTTGGAAGTAAAA 321
```

RESULT

```
ID   T87441 standard; cDNA; 321 BP.
AC   T87441;
DT   12-JAN-1998 (first entry)
KW   TNF; tumour necrosis factor; Crohn's disease; cA2 antibody; ss.
OS   Synthetic.
FH
PN   EP-872418-A1.
PD   12-AUG-1997.
PR   18-MAR-1991; 670827.
PR   18-MAR-1991; US-670827.
PR   18-MAR-1991; US-853606.
PR   18-MAR-1993; US-670827.
PR   26-JAN-1993; US-010606.
PR   26-JAN-1993; US-013413.
PA   (CNTC) CENTOCOR INC.
PA   (UYNY-) UNIV NEW YORK MEDICAL CENT.
PI   Vilcek J; Le J, Siegel SA;
PI   Daddona P; Ghrayeb J; Knight D; Le J, Siegel SA;
DR   WPI; 97-414547/38.
DR   P-PSDB; W28531.
PT   Treatment of Crohn's disease - by administering humanised cA2
PT   antibody specific for tumour necrosis factor
PS   Disclosure; Fig 16A; 87pp; English.
CC   The cA2 antibody may be administered for treating
CC   TNF-alpha mediated Crohn's disease in a human.
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Right column

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CC   The anti-TNF chimeric antibody competitively inhibits binding of
CC   TNF to monoclonal antibody cA2. The anti-TNF antibody does
CC   not bind to one or more epitopes in amino acids 1-13, 37-42,
CC   49-57 or 155-157 of MTNF, but does bind to one or more epitopes
CC   included in amino acids between 87-108 or both 87-108 and 59-80
CC   of MTNF.
SQ   Sequence 321 BP; 83 A; 72 C; 77 G; 89 T;

Query Match            100.0%;  Score 321;  DB 35;  Length 321;
                       Best Local Similarity 100.0%;  Pred. No. 9.02e-208;
Matches  321;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Db    1 gcacctctgactcagcctccaccgtgtcagggagaaagtcagt 60
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Qy    1 GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGACTCCAGGAGACAGAGTCAGT 60

Db  121 aatggttcctcaggccactcagcctcctgctcttcatctggctccctcc 180
        |||||||||||||||||||||||||||||||||||||||||||||||||
Qy  121 AATGGTTCCTCAGGCCACTCACCTCTCATGATATGTCTTCAGCTGGATCCCTCC 180

Db  181 agttcagcggcagtgatccaacgattacccaccgctcctggctcctc 240
        |||||||||||||||||||||||||||||||||||||||||||||||
Qy  181 AGGTTCAGTGGCAGTGGATCAGGTACAGATTATTACTGTCAACAACGTGGAGACT 240

Db  301 ggacaaattggaagtaaaa 321
        ||||||||||||||||||||
Qy  301 GGGACAAATTTGGAAGTAAAA 321

RESULT 3
ID   M90300 standard; DNA; 1395 BP.
AC   M90300;
DT   1-NOV-1999 (first entry)
KW   Recombinant DNA; chimeric monoclonal antibody; light chain; heavy chain;
KW   variable region; human carcinoembryonic antigen; cell line CE25.
FT   cds
FT                    /tags=a
FT   781  987
FT                    /tag=b
FT   intron
FT   733..1320
FT   cds
FT                    location/Qualifiers
FT   733..1320
PN   EP-323806-A.
PD   1-NOV-1999.
PR   28-DEC-1988; 810898.
PR   05-JAN-1988; GB-00077.
PA   (CESS-) CENTRO CHem-detergent AG.
PA   Hachman N. Gill; de Winter REJ, Wagner K, Heusser C;
PR   WPI; 89-200701/28.
DR   P-PSDB; C28519.
PT   Chimeric monoclonal antibody to human carcinoembryonic antigen
PT   - consisting of variable regions of mouse origin and human constant
PT   region, useful for diagnosis and therapy.
PS   Claim 25; 2pp; English.
CC   The recombinant DNA is an insert coding for a light chain murine
CC   variable region, chimeric antibody CE25 murine antigen and human constant
CC   originates from genomic DNA of the cell line CE 25. See also P90479.
SQ   Sequence 1395 BP;  397 A;  240 C;  240 T;  482 T;

Query Match             90.7%;  Score 291;  DB 1;  Length 1395;
                       Best Local Similarity 95.3%;  Pred. No. 4.65e-186;
Matches  306;  Conservative 0;  Mismatches 15;  Indels 0;  Gaps 0;

Db 1000 gacatctgacctcagctccagccatcctgtctgtgactccaggagac 1059
        |||||||||||||||||||||||||||||||||||||||||||||||
Qy    1 GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGACTCCAGGAGACAGAGTCAGT 60
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Left column:

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Db  1060 tctctcgcagggcagcagacagcccagcctccagccacctcgtgctctcgggggaaagagactct 1119
         ||||||||||||||||||| ||||||||||||| |||||||||||||||||||||||||
Qy    61 TTCTCTCGCAGGGCCAGCTCAGTTCGTTGGCTCAAGCATCCACTGGTATCAGCAAGAACA 120

Db  1120 aacggttcccaggaagccatcagggatgtcactgaaccatccacgtataacccaaagaa 1179
         |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy   121 AATGGTTCCCCAGGAAGCCTTCTCATAGTGTCCTCTGCATATATCTGGGATCCCTTC 180

Db  1180 aggttctggctggtcgacaatggatcggggatggggaaaacc 1239
         ||||||||||||||||||||||||||||||||||||||||||
Qy  181 AGGTTTAGTGGCAGTGGATCAGGGACAGATTTTACTCTCACCATCACCAGTGTGCAGCCT 240

Db  1240 gaagatatggagtcgagactgatcaggacgctcaactcaggctcaagtactataggggccct 1299
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  241 GAAGATATTGCAGATTATTACTGTCAACAAGGTCATAGCTTGCCATTCACGTTCGGCTCG 300

Db  1300 gggacaagttggaataaa 1320
         ||||||||||||||||||
Qy  301 GGGACAAATTTGGAAGTAAA 321
```

```
RESULT   4
AC  V12262;
AC  V12262:
DT  31-DEC-1997.
DE  Monoclonal antibody, light chain against type II phospholipase A2
DE  (inhibition; cisplatin; Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin;
KW  amelioration; kidney disorder; nephrotoxicity; anticancer; ds.
Key   Location/Qualifiers
FH
FT  CDS                1..381
FT                     /note="product='Monoclonal antibody 12H5 light chain'"
FT                     /note "no stop codon given"
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RESULT
AC  W09745427;A1.
DT  31-DEC-1997.
PN  27-JUN-1997; JO2241X.
PR  19-SEP-1996; JP-167235.
PA  (YAMA) YAMANOUCHI PHARM CO LTD.
PI  Kitazawa H; Mesuno Y; Takasaki J;
DR  WPI:98-076914/07
DR  P-PSDB; W41176.
```

Right column:

```
Db    61 gacatctgccgactcagtccagcctccagccacctcgtgctctcggggggaaagagagtct 120
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Qy     1 GACATCTTCCTGACTCAGTCTCCAGCCACCCTGT 60

Db   121 tctctcgcagggcagccagttcgtcggcctcagcatccactggtatcagcaagaacca 179
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Qy    61 TTCTCTCGCAGGGCCAGCAGTTCGTTGGCTCAAGCATCCACTGGTATCAGCAAGAACA 120

Db   181 aatggttccccaggaagccttctcatagtgtcctctgcatatatctgggatcccttc 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 AATGGTTCCCCAGGAAGCCTTCTCATAGTGTCCTCTGCATATATCTGGGATCCCTTC 180

Db   241 aggttctggctggtcgacaatggatcggggatggggaaaacc 300
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Qy   181 AGGTTTAGTGGCAGTGGATCAGGGACAGATTTTACTCTCACCATCACCAGTGTGCAGCCT 240

Db   301 gagatattgcagattatactgtcaacaaggtcatagcttgccattcacgttcggctcg 360
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Qy   241 GAAGATATTGCAGATTATTACTGTCAACAAGGTCATAGCTTGCCATTCACGTTCGGCTCG 300

Db   361 gggacaaatttggaagtaaa 380
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Qy   301 GGGACAAATTTGGAAGTAAA 320
```

```
RESULT  5
AC  V26766 standard; cDNA; 321 BP.
AC  V26766;
AC  V26766:
DT  14-SEP-1998. (first entry)
DE  Single chain antibody variable region, cDNA.
DE  Single chain antibody; scFv; monoclonal antibody;
KW  trop-2; gp54; antigen; cancer marker; bladder cancer;
KW  breast cancer; cervix cancer; prostate cancer; metastasis;
KW  diagnosis; therapy; immunotherapy; ds.
OS  Mus sp.
FH  Key          Location/Qualifiers
FT  CDS          10..321
FT               /tag= a
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RESULT
AC  W09812237;A1.
DT  26-MAR-1998.
PN  19-SEP-1997;
PR  19-SEP-1997; US-936320.
PA  (DIAC) DIAGNOCURE INC.
PA  (DIAC) DIAGNOCURE INC.
PI  Darveau A; Frodis W;
DR  WPI:98-263320.
DR  P-PSDB; W26735.
```

RESULT 6

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ID   Q43243 standard; DNA; 321 BP.
AC   Q43243;
DT   13-OCT-1993 (first entry)
DE   B-B10 MAb L chain V region DNA.
KW   Complementarity-determining regions; CDR; humanised; antibody; hIL2R;
KW   human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
KW   monoclonal antibody; B-B10; interleukin-2 receptor (hIL2R); variable; V;
KW   framework; framework; plasmid; heavy; H; light; L; ss.
OS   Mus musculus
OC   Mus musculus
PN   WO9311789-A.
PD   10-JUN-1993
PF   03-DEC-1992; JO158319
PR   06-DEC-1991; DE-9141856
PA   (INNO-) INNOTHERAPIE LAB.
PA   (INNO-) INNOTHERAPIE LAB.
PA   (SOMU) SUMITOMO PHARM CO LTD.
PI   Jurgen H. Nakami T. Noguchi H.   Wildenes J.
PI   WPI 93-197057/24.
DR   P-PSDB: R37610
```

CC   Humanised antibody comprising - CDR region of mouse MAB B-B10
CC   specific for IL-2 receptor useful for treating carcinoma
CC   expressing IL-2 receptor
CC   The sequences given in Q43242+43 encode the heavy (H) and light (L)
CC   chain variable (V) regions of the murine anti-human IL-2 receptor
CC   monoclonal antibody (MAb) B-B10 respectively. This MAb was used in
CC   the construction of a humanised antibody (Ab) which binds specifically
CC   to human interleukin (IL)-2 receptor (hIL2R). The complementarity-
CC   determining regions (CDR) of B-B10 were identified from the V region
CC   (see also R37599-04). The hIL2R MAb is antagonistic to the binding
CC   of IL-2 to the IL-2 receptor on human T-cells. It also inhibits
CC   the proliferation of T-cells. The human Ab chain framework variable
CC   (V) region of the B-B10 Ab was cloned by PCR and sequenced (see also
CC   Q43226-32 and Q43233-36). A human Ab with high levels of amino acid
CC   homology to B-B10 was selected to provide the humanised Ab
CC   framework of the framework to B-B10 V region CDR were a
CC   part of the framework was cloned. Several kinds of the humanised B-B10
CC   framework and Ab was bound with the B-B10 V region CDR was constructed
CC   synthesised and a plasmid expressing humanised B-B10 was constructed.
SQ   Sequence 321 BP; 82 A; 74 C; 81 G; 84 T;

```
Query Match   86.9%;  Score 279;  DB 7;  Length 321;
Best Local Similarity   86.9%;  Pred. No. 2.17e-177;
Matches  300;  Conservative  0;  Mismatches 21;  Indels  0;  Gaps  0;

db    1  gacatctcctgacctctgctcaccccagccatccagctgactcagtctccatccagcagt  60
         ||||||||||||||||||| ||||||| || |||||||| || ||| ||||||||||||
Qy    1  GACATCTCTGACCTCAGTCTCCAGCCATCCAGCCATCCTGTCTGCATCTGTAGGAGACAGAGTCAGT  60
```

```
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Oy   61  tctcctcgagcggccagctccagcaatcggcgacacctaccatacacaccgtcaagaaca 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Oy   61  TTCTCCTGCAGGGCCAGTCAGTTCCTTGGCTCAAGCATCCAGTCATCGACCAAGAACAA 120
```

```
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Oy  121  aatggttctccaagctcctcataaaagtacgttctactaggatcccctggatccctttcc 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Oy  121  AATGGTTCTCCAAGCTCCTCAAGCTATCCTCTGTCTATCGTCTGGGATCCCTTTCC 180
```

```
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Oy  181  agtttctcgggtcgcggatcaagacattctactgcctgcaggttggagatct 240
         ||||||||||||||||||||||||||||||||||||||||||
Oy  181  AGGTTTAGTGGCAGTGGATCAGGGACAGGATTTTACTCTTACCACCAACACTGGGAGTCT 240
```

```
         |||||||||||||||||||||||||||||||||||||||||||||||
Oy  241  gaagatattgcagatttattctgccaaaagtacgaactccaaacgactggtcgctcgtct 300
         |||||||||||||||||||||||||||||||||||||
Oy  241  GAAGATATTGCAGATTATTACTGTCAACAAGCTAACAGCTATCCGCTCACGTTCGGCTCG 300
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```
         |||||||||||||||||
Oy  301  ggaccaaagttgaaataaa 321
         ||||||||||||
Oy  301  GGGACAAAGTTGGAAGTAAA 321
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RESULT 7

```
ID   V26770 standard; cDNA; 720 BP.
AC   V26770;
DT   04-SEP-1998 (first entry)
DE   Anti-gp54 MAb 48-127; scFv cDNA.
KW   Single chain antibody; scFv; monoclonal antibody; MAB; 48-127;
KW   trop-2; gp54; antigen; cancer marker; bladder cancer;
KW   diagnosis; therapy; immunotherapy; ds
OS   Chimeric - Mus sp.
OS   Chimeric - Synthetic
FH   Key              Location/Qualifiers
FT   CDS              3..720
FT                    /gene       a
PN   WO9812227-A1.
PD   26-MAR-1998
PF   19-SEP-1997; CA0690
PI   19-SEP-1996; US-026320.
PA   (DIAG-) DIAGNOCURE INC.
PI   (DIAG-) DIAGNOCURE INC.
DR   WPI 98-212717/19.
DR   P-PSDB: W26770.
```

CC   Novel gp54 antigen antibodies to gp54 antigen - used for the detection
CC   of cancers and metastases and for therapy of cancers expressing the
CC   gp54 antigen.
CC   This cDNA sequence codes for a novel single chain antibody
CC   (scFv; see W26759) the heavy chain variable region
CC   (scFv; see W26759) that comprises the heavy chain variable region
CC   joined by a peptide linker to the light chain variable region. The
CC   light chain variable region (see W26755) of 48-127 via a peptide
CC   linker. It is obtained by PCR amplification of 48-127 light chain
CC   variable region (see W26755). The scFv product is a single chain
CC   ligation of amplified fragments. The construct has been cloned
CC   into vector pDIAG-CMV, and modified the scFv expressed in transfected COS-7
CC   cells. Antibodies to the gp54 antigen are useful in detecting
CC   cancer marker expressed at the surface of bladder, breast, uterine
CC   and prostate cancers. It can be used to detect cancers and
CC   metastases that express gp54 antigen on the surface. In cervix
CC   cancers, and may be linked to specific toxins for use in cancer
CC   therapy. Such scFvs are not immunogenic and are distributed and
CC   cleared by gp54-bearing target cells more quickly than conventional
CC   antibodies.
SQ   Sequence 720 BP; 178 A; 160 C; 200 G; 182 T;

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Query Match   86.3%;  Score 277;  DB 44;  Length 720;
Best Local Similarity   93.4%;  Pred. No. 6.04e-176;
Matches  298;  Conservative  0;  Mismatches 21;  Indels  0;  Gaps  0;

db  402  gacttatgatgacgcaatctcagccagagaaaaagagtcagt 461
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Oy    1  GACATCTCTGACCTCAGTCTCCAGCCATCCAGTCTCCAGGGAGAAAGAGTCAGT  60
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Left column

JOURNAL   Eur. J. Immunol. (1991) in press
REFERENCE 2 (bases 1 to 318)
AUTHORS   Kaartinen,M.
TITLE   Direct Submission
JOURNAL   Submitted (02-OCT-1991) EMBL Data Library by: Kaartinen M.,
           University of Helsinki, Dept. of Bacteriology Haarthaninkatu 3
           SF-00290 Helsinki Finland

FEATURES   Location/Qualifiers
     source   1..318
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /chromosome="12"
                     /cell_type="B lymphocyte"
                     /clone="VH16C10"
     misc_feature   <1..18
                     /gene="V(H)J307"
                     /note="leader region"
     CDS   <1..>318
                     /gene="V(H)J307"
                     /codon_start=1
                     /product="immunoglobulin heavy chain"
                     /protein_id="CAA42726.1"
                     /db_xref="GI:951248"
                     /db_xref="GI:51248"
                     /translation="YKLSCVASGFTFSDYYVHWVRQPGQGLEWLGVWAEILKSNNYATHY
                     QSPEKGLEWVAEILKSNNYATHYASVKGRFTISRDDSKSSVYLQMNNLRAEDTGTYYCTSV
                     YCTKT"
     gene   1..318
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     misc_feature   19..>318
                     /gene="V(H)J307"
                     /note="V region"

BASE COUNT   90 a   60 c   81 g   87 t
ORIGIN

Query Match 72.8%; Score 260; DB 32; Length 318;
Best Local Similarity 100.0%;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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db  19 GAAGTCGAACCTGGAGGTTCTGAGGGTGGTGCCAACCTGAGGATTCATGAAAACTC  78
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Qy   1 GAAGTCGAACCTGGAGGTTCTGAGGGTGGTGCCAACCTGAGGATTCATGAAAACTC  60

db  79 TCCTGTGTTCCCTCTGGATTCACTTTCAGTGACTACTACGTGCATTGGGTCCGCCAGTCT 138
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  61 TCCTGTGTTCCCTCTGGATTCACTTTCAGTGACTACTACGTGCATTGGGTCCGCCAGTCT 120

db 139 CCAGAGAAGGGGTTGGAGTGGCTGGGAGTTGTAGCAGATATTAGTGAAATCTAATAATTATCACA 198
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 CCAGAGAAGGGGTTGGAGTGGCTGGGAGTTGTAGCAGAATTGTAATTATTTATCACA 180

db 199 CATTATCGCAGGCTGCTGAAGGGAGGTTCACCATCTCAAGAGATGAT CAAAAGTAGT 258
        |||||||||||||||||||||||||||||||||||||||||||||
Qy 181 CATTATCGCAGGCTGCTGAAGGGAGGTTCACCATCTCAAGAGATGATCAAAAGTCGT 240

db 259 GTCTACCTGCAAATGAACAACTTGCGTCGGAGGACACTGGGCATTTATTACTGTACAGG 318
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Qy 241 GTCTACCTGCAAATGAACAACTTAAGAACTGAAGACACTGGGCTTTATTACTGTTCAGG 300
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RESULT 9
LOCUS   MMJ73591   354 bp   mRNA   ROD   09-DEC-1996
DEFINITION Mus musculus immunoglobulin H23 rearranged heavy chain variable
           region (IgGVH) mRNA, partial cds.
ACCESSION MMJ73591
NID   g1710422
VERSION   J73591.1 GI:1710422
KEYWORDS   .
SOURCE   house mouse.
ORGANISM   Mus musculus
           Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
           Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.

Right column

JOURNAL   Eur. J. Immunol. (1991) in press
REFERENCE 2 (bases 1 to 354)
AUTHORS   Fiorentini,S., Matzak,E., Reitz,M.S. Jr., Gallo,R.C., Keydar,I.
           and Watkins,B.A.
TITLE   Humanization of an antibody recognizing a breast cancer specific
           epitope
JOURNAL   Immunotechnology (1996) In press
REFERENCE AUTHORS   Fiorentini,S., Matzak,E., Reitz,M.S. Jr., Gallo,R.C., Keydar,I.
           and Watkins,B.A.
TITLE
JOURNAL   Submitted (07-OCT-1996) Lab of Tumor Cell Biology, National Cancer
           Institute, 37 Convent Drive, Room 6A11, Bethesda, MD 20892-4255,
           USA

FEATURES   Location/Qualifiers
     source   1..354
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                     /strain="BALB/c"
                     /db_xref="taxon:10090"
                     /tissue_type="hybridoma"
     V-region   1..354
                     /gene="IgGVH"
     gene   1..354
                     /gene="IgGVH"
     CDS   1..354
                     /gene="IgGVH"
                     /note="recognizes breast cancer associated antigen Muc-1"
                     /codon_start=1
                     /product="immunoglobulin H23 rearranged heavy chain
                     variable region"
                     /protein_id="AAB38390.1"
                     /db_xref="GI:1710423"
                     /db_xref="GI:1710423"
                     /translation="LKYKLVSEGGGLVQPGRSMKLSCVASGFTFSNYWMNWVRQSPEX
                     XXXXXXXXXXXXXXXXXXXXGRFTISRDDSKSSVYLQMNNLRAEDTGITYCTSV
                     IGFAYWGQGTLVTVSS"

BASE COUNT   91 a   69 c   98 g   96 t
ORIGIN

Query Match 72.8%; Score 260; DB 32; Length 354;
Best Local Similarity 94.2%; Pred. No. 329-193;
Matches 277; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Qy   1 GAGGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGGAGATCCATGAAAACTC  60

db  64 TCCTGTGTTCGTCTGGATTCACTTTCAGTAACTACTGGTCAACTAATATCATCAACA 123
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Qy  61 TCCTGTGTCCCTCTGGATTCACTTTCAGTGATACTGGATGTCACTAACTATATCATCAACA 120

db 124 CCAGAGAAGGGGCTGGAGTGGGTCGCAGATTAATAGTAATGGTAGTAATACCAACA 180
        ||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 CCAGAGAAGGGGCTGGAGTGGGTCGCAGAATTAATAGTAATGGTAGTAATACCTCAACA 180

db 184 CATTATGCCGAGGGTTGAAGGGCCGATTCACCATCTCAAGAGATGATTCTCAAAAGTAGT 243
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Qy 181 CATTATGCCGAGTCTGTGAAGGGCCGATTCACCATCTCAAGAGATGATTCTCAAAAGTAGT 240

db 244 GTCTACCTGCAAATGAACAACTTAAGAGCTGAAGACACTGGGCATTTATTACTGT 297
        |||||||||||||||||||||||||||||||||||||||||||
Qy 241 GTCTACCTGCAAATGAACAACTTAAGAGCTGAAGACACTGGGCATTTATTACTGT 294
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RESULT 10
LOCUS   MUSIGHT   427 bp   mRNA   ROD   22-MAY-1991
DEFINITION Mouse Ig mu-chain (J606 family) mRNA V-region (V2), from hybridoma
ACCESSION MC-1004 mu
NID   M17167.1 GI:195413
VERSION   g195413
           M17167.1 GI:195413
KEYWORDS   J-region, V-region; immunoglobulin heavy chain; immunoglobulin.

SOURCE   mu-chain,
              Mouse (BALB/c) anti-bloodgroup A hybridoma, cDNA to mRNA, clone
              BC-1004-mu.
ORGANISM   Mus musculus
              Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
              Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
              Murinae; Mus (Mus 427)
REFERENCE   1 (bases 1 to 427)
AUTHORS   Chen,H.-T., Kabat,E.A., Lundblad,A. and Ratcliffe,R.M.
TITLE   Nucleotide and translated amino acid sequences of cDNA coding for
              the mu-chain of the light and heavy chains of the anti-mouse
              hybridoma antibodies to blood group A and B substances
JOURNAL   J. Biol. Chem. 262, 13579-13583 (1987)
MEDLINE
COMMENT   Draft entry and printed copy of sequence for [1] kindly provided by
              E.A. Kabat, 04-AUG-1987.
FEATURES   Location/Qualifiers
     source   1..427
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
     sig_peptide   1..67
                     /note="Ig mu-chain"
     CDS   1..>427
                     /note="Ig mu-chain precursor V-region (VJ)"
                     /codon_start=1
                     /gcode=1
                     /db_xref="GI:553990"
                     /db_xref="GI:553990"
                     /translation="METGLRWLFLVVFLAGVQSRVLRLSSGLVQPGGSRKLSCAAS
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                     QMNSLRAE"
     mat_peptide   68..>427
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                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
BASE COUNT   112 a   85 c   113 g
ORIGIN   Chromosome 12.

Query Match   72.8%; Score 260; DB 32; Length 427;
Best Local Similarity 96.9%; Pred No.3;2e-193;
Matches 308; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Db   68 GAAGCGAACCTTGAGGAGCTTGAGGAGGCTGGTGCAACTCAGGATCCATGAAACTC 127
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1 GAAGCGAACCTTGAGGAGCTTGAGGAGGCTGGTGCAACTCAGGATCCATGAAACTC 60

Db   128 TCCTGTGCTGCCTCTGGATTCATTTTCAGTGACGCCGATGGACTGTGGGTCCCAGTCT 187
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   61 TCCTGTGCTGCCTCTGGATTCATTTTCAGTGACGCCGATGGACTGTGGGTCCCAGTCT 120

Db   188 CCGAGAAGGGGCCTTGAGTGGGTTGCTCACCTAGAAGCAAAGTCGATAAATCATGCAACA 247
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 CCGAGAAGGGGCCTTGAGTGGGTTGCTCACCTAGAAGCAAAGTCGATAAATCATGCAACA 180

Db   248 TACTAATACGAGTCTGTGAAAGGGAGGCATGATTCCAAAGAAGAAT 307
           |||||||||||||||||||||||||||||||||||||||||||||||
Qy   181 CATTATGCGGATCCTGTGAAAGGGAGGCATGATTCCAAAGAAGAAT 240

Db   308 CCTCACCTGCAAATGAACAGCCTGAGAGCTGAAGACTGGTCCCATTGATTCACTACAGG 367
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   241 GTCTACCTGCAAATGAACAGCCTGAGAGCTGAAGACTGGTCCCTTTATTACTGGTCCAGG 300

Db   368 GATTACTACGGTGCAGGAGTTGCTTACTGGGGCCAAGGGACTCTGTCTC 423
           ||||||||||||||||||||||||||||||||||||||||||||||||
Qy   301 AATTACTACGGTGCAGGAGTTGCTTACTGGGGCCAAGGGACTCTGTCTC 356

RESULT 11
LOCUS   MUS13USA   305 bp   mRNA   ROD   04-AUG-1994
DEFINITION Mouse Ig active V-region (GAC1) mRNA V-region, from hybridoma
ACCESSION   M32053
NID   G1:195976
VERSION   M32053.1   G1:195976
KEYWORDS   V-region; immunoglobulin heavy chain; processed gene.

───

SOURCE   Mouse (strain A/J), cDNA to mRNA, anti-GAC hybridoma 66.3E3.
ORGANISM   Mus musculus
              Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
              Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
              Murinae; Mus (Mus 427)
REFERENCE   1 (bases 1 to 305)
AUTHORS   Jarvis,C.D., Cannon,L.E. and Stavnezer,J.
TITLE   V-region sequence of a mouse Ig response to a streptococcal carbohydrate
JOURNAL   Chem. 262, 4213-4220 (1989)
MEDLINE
FEATURES   Location/Qualifiers
     source   1..305
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
     intron   <1..11
                     /note="Ig H-chain V-region intron"
     exon   85..a   55 c   85 g   0;
BASE COUNT
ORIGIN   Chromosome 12.

Query Match   72.0%; DB 32; Length 305;
Best Local Similarity 93.9%; Pred No.3;8e-190;
Matches 275; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db   13 GAAGTGAAGCTTGAGGAGTCTGGAGGAGTGGCTGGTGCAACTCAGGATCCATGAAACTC 72
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1 GAAGTGAAGCTTGAGGAGTCTGGAGGAGTGGCTGGTGCAACTCAGGATCCATGAAACTC 60

Db   73 TCCTGTGCTGCCTCTGGATTCACTTTCAGTAACTACGGATCCATGAGCTGGGTCCGCCAGTCT 132
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   61 TCCTGTGCTGCCTCTGGATTCATTTTCAGTAACTACGCCATGAGCTGGGTCCGCCAGTCT 120

Db   133 CCAGAGAAGGGGTTGGAGTGGGTTGCTGAAATTAGATTGAAATCTAATAATTATGCAACA 192
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 CCAGAGAAGGGGTTGGAGTGGGTTGCTGAAATTAGTAGTAGTGGTGGTAGCACCTACTAT 180

Db   193 CATTATGCGGATCCTGTGAAAGGGAGGCATGATTCCAAAGAAGAAT 252
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Qy   181 CATTATGCGGATCCTGTGAAAGGGAGGCATGATTCCAAAGAAGAAT 240

Db   253 GTCTACCTGCAAATGAACAACTTACAGCTGAGGACTGGTGATTTATTACTG 305
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   241 GTCTACCTGCAAATGAACAACTTACAGCTGAGGACTGGTGATTTATTACTG 293

RESULT 12
LOCUS   MUS13USA   306 bp   mRNA   ROD   15-JUN-1990
DEFINITION Mouse Ig active H-chain (GAC1) mRNA V-region. from hybridoma
              80.1B5. partial cds.
ACCESSION   M32046
NID   G1:195971
VERSION   M32046.1   G1:195971
SOURCE   Mouse (strain 80.1B5), cDNA to mRNA, anti-GAC hybridoma 80.1B5.
ORGANISM   Mus musculus
              Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
              Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
              Murinae; Mus (Mus 427)
REFERENCE   1 (bases 1 to 306)
AUTHORS   Jarvis,C.D., Cannon,L.E. and Stavnezer,J.
TITLE   Mouse antibody response to group A streptococcal carbohydrate
JOURNAL   Chem. 143, 4213-4220 (1989)
MEDLINE
FEATURES   Location/Qualifiers
     source   1..306
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
     intron   12..>306
                     /note="Ig H-chain V-region intron. X"
     exon   85..a   56 c   85 g   0;
BASE COUNT

ORIGIN   Chromosome 12.

Query Match   72.0%; Score 257; DB 32; Length 306;
Best Local Similarity   93.9%; Pred. No. 1.13e-190;
Matches   275; Conservative   0; Mismatches   18; Indels   0; Gaps   0;

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Db    13 GAAGTGAAGCTGGAGAGCTCGAGAGCTTGGTGCAACCTGGAGGATCCATGAAACTC  72
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Qy     1 GAAGTGAAGCTGGAGAGCTCGAGAGCTTGGTGCAACCTGGAGGATCCATGAAACTC  60

Db    73 TCCTGTGTTGCCTCTGGATTCACTTTCAGTAACTACTGGATGAACTGGGTCCGCCAGTCT 132
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    61 TCCTGTGTTGCCTCTGGATTCACTTTCAGTAACTACTGGATGAACTGGGTCCGCCAGTCT 120

Db   133 CCAGAGAAGGAGCTGGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCACA 192
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Qy   121 CCAGAGAAGGAGCTGGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCACA 180

Db   193 CATTATCCGGAGTCTGCAAATGAACAGCTTAAGGCTGAAGGACACTGGAATTTATACTG 252
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   181 CATTATCCGGAGTCTGCAAATGAACAGCTTAAGGCTGAAGGACACTGGAATTTATACTG 240

Db   253 GTCTACCTGCAAATGAACAGCTTAAGAACTGAAGACACTGGCGTTTATTACTG 305
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Qy   241 GTCTACCTGCAAATGACCACTTAAGAACTGAAGACACTGGCGTTTATTACTG 293
```

RESULT   13
LOCUS   MUSIGHRT   314 bp   mRNA   ROD   15-JUN-1990
DEFINITION Mouse Ig active H-chain (GACI) mRNA V-region, from hybridoma
           68.2D8, partial cds.
ACCESSION M32044
NID   g195969
VERSION   M32044.1 GI:195969
SOURCE   Mouse (strain A/J), cDNA to mRNA, anti-GAC hybridoma 68.2D8.
  ORGANISM Mus musculus
           Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
           Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
           Murinae; Mus
REFERENCE 1 (bases 1 to 314)
  AUTHORS Darnell,J.E., Laffer,J., and Stavnezer,J.
  TITLE   Mouse antibody response to group a streptococcal carbohydrate
  JOURNAL J.Immunol. 143, 4213-4220 (1989)
  MEDLINE 90079031
FEATURES   Location/Qualifiers
     source   1..314
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
     intron   <1..11
                     /note="Ig H-chain V-region intron"
     exon   12..>314
                     /note="Ig H-chain, X"
BASE COUNT   88 a   58 c   86 g   82 t
ORIGIN   Chromosome 12

Query Match   72.0%; Score 257; DB 32; Length 314;
Best Local Similarity   93.9%; Pred. No. 1.13e-190;
Matches   275; Conservative   0; Mismatches   18; Indels   0; Gaps   0;

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Db    13 GAAGTGAAGCTGGAGAGCTCGAGAGCTTGGTGCAACCTGGAGGATCCATGAAACTC  72
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Qy     1 GAAGTGAAGCTGGAGAGCTCGAGAGCTTGGTGCAACCTGGAGGATCCATGAAACTC  60

Db    73 TCCTGTGTTGCCTCTGGATTCACTTTCAGTAACTACTGGATGAACTGGGTCCGCCAGTCT 132
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Qy    61 TCCTGTGTTGCCTCTGGATTCACTTTCAGTAACTACTGGATGAACTGGGTCCGCCAGTCT 120

Db   133 CCAGAGAAGGAGCTGGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCACA 192
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 CCAGAGAAGGAGCTGGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCACA 180

Db   193 CATTATCCGGAGTCTGCAAATGAACAGCTTAAGGCTGAAGGACACTGGAATTTATACTG 252
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Qy   181 CATTATCCGGAGTCTGCAAATGAACAGCTTAAGGCTGAAGGACACTGGAATTTATACTG 240

Db   253 GTCTACCTGCAAATGAACAGCTTAAGAACTGAAGACACTGGCGTTTATTACTG 305
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Qy   241 GTCTACCTGCAAATGACCACTTAAGAACTGAAGACACTGGCGTTTATTACTG 293
```

RESULT   14
LOCUS   MMD01110   366 bp   mRNA   ROD   12-SEP-1994
DEFINITION Mus musculus BALB/c anti-glycophorin A type M Ig heavy chain mRNA,
           partial cds.
ACCESSION D01110
NID   g414566
VERSION   D01110.1 GI:414566
KEYWORDS   .
SOURCE   house mouse.
  ORGANISM Mus musculus
           Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
           Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
           Murinae; Mus
REFERENCE 1 (bases 1 to 366)
  AUTHORS Spitalnik,S.L.
  TITLE   Restricted VH usage by murine hybridomas directed against the human
           M, but not M, antigen
  JOURNAL Unpublished
REFERENCE 2 (bases 1 to 366)
  AUTHORS Spitalnik,S.L.
  TITLE   Direct Submission
  JOURNAL Submitted (03-NOV-1993) Steven L. Spitalnik, Department of Pathol.
           and Lab. Medicine, University of Pennsylvania, 36th & Hamilton
           Walk, 322 John Morgan Building, Philadelphia, PA 19104, USA
FEATURES   Location/Qualifiers
     source   1..366
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /db_xref="taxon:10090"
                     /cell_line="425"
                     /cell_type="hybridoma"
     CDS   1..>366
                     /standard_name="anti-glycophorin A type M, antibody 425"
                     /codon_start=1
                     /product="immunoglobulin heavy chain"
                     /protein_id="AAA21378.1"
                     /db_xref="PID:g145657"
                     /db_xref="GI:145657"
                     /translation="EVQLVESGGGLVQPGGSMKVSCIASGFTFSHYWMNWVRQSPEKG
                     LEWVAEIRLRSDNYATHYAESVKGRFTISRDDSKSSVYLQMNNLRAEDTGIYYCTRAG
                     TGYHYDMDWGQGTSVTVIS"
BASE COUNT   100 a   99 g   99 c   92 t
ORIGIN

Query Match   72.0%; Score 257; DB 32; Length 366;
Best Local Similarity   93.9%; Pred. No. 1.13e-190;
Matches   284; Conservative   0; Mismatches   27; Indels   0; Gaps   0;

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Db     1 GAAGTGCAGCTGGTGGAGTCTGGAGGAGGCTTGGTCCAACCTGGAGGGTCCATGAAAGTC  60
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Qy     1 GAAGTGAAGCTGGAGAGCTCGAGAGCTTGGTGCAACCTGGAGGATCCATGAAACTC  60

Db    61 TCCTGTATTGCCTCTGGATTCACTTTCAGTCACTACTGGATGAACTGGGTCCGCCAGTCT 120
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Qy    61 TCCTGTGTTGCCTCTGGATTCACTTTCAGTAACTACTGGATGAACTGGGTCCGCCAGTCT 120

Db   121 CCAGAGAAGGGCCTGGAGTGGGTAGCAGAAATCAGATTGAGATCTGATAATTATGCAACA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 CCAGAGAAGGAGCTGGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA 180

Db   181 CATCATGCGGAGTCTGTGAAAGGGAGGTTCACCATCTCAAGAGATGATTCCAAAAGTAGT 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   181 CATTATCCGGAGTCTGCAAATGAACAGCTTAAGGCTGAAGGACACTGGAATTTATACTG 240
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Qy   181 CATTATGCGGAGTCTGTGAAAGGGGAGGTTCACCATTCTCAAGAGAGATGATTCCAAAGTGCT 240
             |||||||||||||||||||||||||||||||||| |||||||||||||| ||||
Db   241 GTCTACCTGCAAATGAACAACTTAAGAGCTGAAGACACTGCCATTTATTACTGACCAGG 300
             |||||||||| |||||||| ||||||| |||||||||||||| |||||||| |||||
Qy   241 GTCTACCTGCAAATGACCGACTTAAGACACTGAAGACACTGCGCGTTATTACTGTTCCAGG 300

Db   301 CGGGGCTCACGG 311
             |||||||||||
Qy   301 AATTACTACGG 311


RESULT  15
LOCUS       MUSIGHRV          314 bp    mRNA           ROD     15-JUN-1990
DEFINITION  Mouse Ig active H-chain (GAC1) mRNA V-region. from hybridoma
            68.3D3, partial cds.
ACCESSION   M32045
NID         g195970
VERSION     M32045.1  GI:195970
KEYWORDS    V-region; immunoglobulin heavy chain; processed gene
SOURCE      Mouse (strain A/J), cDNA to mRNA, anti-GAC hybridoma 68.3D3.
  ORGANISM  Mus musculus
            Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
            Murinae; Mus
REFERENCE   1  (bases 1 to 314)
  AUTHORS   Jarvis,C.D., Cannon,L.E. and Staenzer,J.
  TITLE     Mouse antibody response to group a streptococcal carbohydrate
  JOURNAL   J. Immunol. 143, 4213-4220 (1989)
  MEDLINE   90079033
FEATURES             Location/Qualifiers
     source          1..314
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     intron          <1..11
                     /note="Ig H-chain V-region intron"
     exon            12..>314
                     /note="Ig H-chain V-region, X"
BASE COUNT       88 a     58 c     85 g     82 t    1 others
ORIGIN          Chromosome 12
Query Match             71.7%;  Score 356;  DB 32;  Length 314;
Best Local Similarity   93.8%;  Pred No. 9.8e-190;
Matches  274;  Conservative   0;  Mismatches  18;  Indels  0;  Gaps   0;

Db    14 AAGTGAGGCTTGAGCAGTCTGGAGAGGCTGTGTCCAACCTGGAAGATCATCGAAACTCT 73
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Qy     2 AAGTGAAGCTTGAGGAGTCTGGAGAGGCCTGGTCAACCTGGAAGATCATCGAAACTCT 61

Db    74 CCTGTGTTGCCTCTGGATTCACTTTCAGTAACTACTGGATGACTGGGTCCGCCAGTCTC 133
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Qy    62 CCTGTGTTGCCTCTGGGATTCATTTCAGTAACTACTGGATGAACTGGGTCCGCCAGTCTC 121

Db   134 CAGAGAAGGACCTGAGTGGGTTGCTGAATTAGATTGAAATCTGATAATTATGCAACAC 193
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Qy   122 CAGAGAAGGGCCTGAGTGGGTTGCTGGTTGCTGAAATTAGATCAAAATCTATTAATCTGCAACAC 181

Db   194 ATTATGCGGAGTCTGTGAAGGAGGTTCACCATCTCAAGAGATGATGTCCAAAAGTAGTG 253
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Qy   182 ATTATGCGGAGTCTGTGAAAGGAGGTTCACCATCTCAAGAGATGATTCCAAAGTGCTG 241

Db   254 TCTACCTGCAAATGAACAGCTTAAGGGCTGAAGACACTGGAATTTATTACTG 305
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Qy   242 TCTACCTGCAAATGACCGACTTAAGACACTGAAGACACTGCGGTTATTACTG 293

Search completed: Wed Sep  8 14:07:17 1999
Job time :1357 secs.
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